

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/441,242B
Source: 1Fw/6
Date Processed by STIC: 7/14/06

ENTERED



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/441,242B

DATE: 07/14/2006

TIME: 09:20:14

Input Set : F:\3589.1017-001 Seq List.txt

Output Set: N:\CRF4\07142006\I441242B.raw

4 <110> APPLICANT: Russo, Giandomenico
 5 Croce, Carlo M.
 7 <120> TITLE OF INVENTION: TCL-1 GENE AND PROTEIN AND RELATED
 8 METHODS AND COMPOSITIONS
 10 <130> FILE REFERENCE: 3589.1017-001
 12 <140> CURRENT APPLICATION NUMBER: 09/441,242B
 13 <141> CURRENT FILING DATE: 1999-11-16
 15 <150> PRIOR APPLICATION NUMBER: 08/330,272
 16 <151> PRIOR FILING DATE: 1994-10-27
 18 <160> NUMBER OF SEQ ID NOS: 12
 20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1324
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Artificial Sequence
 27 <220> FEATURE:
 28 <223> OTHER INFORMATION: cDNA sequence of TCL-1
 W--> 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (49)...(387)
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 34 cttgagagggc tctggctctt gcttcttagg cggcccaggg acgccatg gcc gag tgc 57
 35 Ala Glu Cys
 36 1
 38 ccg aca ctc ggg gag gca gtc acc gac cac ccg gac cgc ctg tgg gcc 105
 39 Pro Thr Leu Gly Glu Ala Val Thr Asp His Pro Asp Arg Leu Trp Ala
 40 5 10 15
 42 tgg gag aag ttc gtg tat ttg gac gag aag cag cac gcc tgg ctg ccc 153
 43 Trp Glu Lys Phe Val Tyr Leu Asp Glu Lys Gln His Ala Trp Leu Pro
 44 20 25 30 35
 46 tta acc atc gag ata aag gat agg tta cag tta cgg gtg ctc ttg cgt 201
 47 Leu Thr Ile Glu Ile Lys Asp Arg Leu Gln Leu Arg Val Leu Leu Arg
 48 40 45 50
 50 cgg gaa gac gtc gtc ctg ggg agg cct atg acc ccc acc cag ata ggc 249
 51 Arg Glu Asp Val Val Leu Gly Arg Pro Met Thr Pro Thr Gln Ile Gly
 52 55 60 65
 54 cca agc ctg ctg cct atc atg tgg cag ctc tac cct gat gga cga tac 297
 55 Pro Ser Leu Leu Pro Ile Met Trp Gln Leu Tyr Pro Asp Gly Arg Tyr
 56 70 75 80
 58 cga tcc tca gac tcc agt ttc tgg cgc tta gtg tac cac atc aag att 345
 59 Arg Ser Ser Asp Ser Ser Phe Trp Arg Leu Val Tyr His Ile Lys Ile
 60 85 90 95
 62 gac ggc gtg gag gac atg ctt ctc gag ctg ctg cca gat gac 387
 63 Asp Gly Val Glu Asp Met Leu Leu Glu Leu Leu Pro Asp Asp

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64 100          105          110
66 tgaatgatgg tcttggcagc acctgtctcc tttcacccca gggcctgagc ctggccagcc 447
67 tacaatgggg atgttggtgt tctgttcacc ttcgtttact atgcctgtgt cttctccacc 507
68 acgctggggg ctgggaggaa tggacagaca gaggatgagc tctaccaggg gcctgcagga 567
69 cctgcctgta gcccactctg ctgcgccttag cactaccact cctgccaagg aggattccat 627
70 ttggcagagc ttcttccagg tgcccagcta tacctgtgcc tcggcttttc tcagctggat 687
71 gatggtcttc agcctctttc tgtcccttct gtccctcaca gcactagtat ttcattgttg 747
72 acaccactc agctccgtga acttgtgaga acacagccga ttcacctgag caggacctct 807
73 gaaaccctgg accagtggtc tcacatgggt ctacgcctgc atgtaaacac gcctgcaaac 867
74 gctgcctgcc ggtaaacacg cctgcaaacg ctgcctgccc gtaaacacgc ctgcaaacgc 927
75 tgccctgcca cacaggttca cgtgcagctc aaggaaaggc ctgaaaggag cccttatctg 987
76 tgcctcaggac tcagaagcct ctgggtcagt ggtccacatc ccgggacgca gcaggaggcc 1047
77 aggccggcga gccctgtgga tgagccctca gaacccttgg cttgcccacg tggaaaagg 1107
78 atagagggtt ggtttccccc ctttatagat ggtcacgcac ctgggtgtta caaagttgta 1167
79 tgtggcatga atactttttg taatgattga ttaaagtcaa gatagtttat ctaacttcgt 1227
80 gcgcaatcag cttctatcct tgacttagat tctggtggag agaagtgaga ataggcagcc 1287
81 cccaaataaa aaatattcat ggaaaaaaaa aaaaaaa 1324

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83 <210> SEQ ID NO: 2

84 <211> LENGTH: 113

85 <212> TYPE: PRT

86 <213> ORGANISM: Artificial Sequence

88 <220> FEATURE:

89 <223> OTHER INFORMATION: cDNA sequence of TCL-1

91 <400> SEQUENCE: 2

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92 Ala Glu Cys Pro Thr Leu Gly Glu Ala Val Thr Asp His Pro Asp Arg
93 1          5          10          15
94 Leu Trp Ala Trp Glu Lys Phe Val Tyr Leu Asp Glu Lys Gln His Ala
95          20          25          30
96 Trp Leu Pro Leu Thr Ile Glu Ile Lys Asp Arg Leu Gln Leu Arg Val
97          35          40          45
98 Leu Leu Arg Arg Glu Asp Val Val Leu Gly Arg Pro Met Thr Pro Thr
99          50          55          60
100 Gln Ile Gly Pro Ser Leu Leu Pro Ile Met Trp Gln Leu Tyr Pro Asp
101 65          70          75          80
102 Gly Arg Tyr Arg Ser Ser Asp Ser Ser Phe Trp Arg Leu Val Tyr His
103          85          90          95
104 Ile Lys Ile Asp Gly Val Glu Asp Met Leu Leu Glu Leu Leu Pro Asp
105          100          105          110

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106 Asp

110 <210> SEQ ID NO: 3

111 <211> LENGTH: 560

112 <212> TYPE: DNA

113 <213> ORGANISM: Artificial Sequence

115 <220> FEATURE:

116 <223> OTHER INFORMATION: genomic sequence of TCL-1

118 <400> SEQUENCE: 3

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119 gtgactgtg agttcccagc agaggccag agtcccggc cggcagccga gggaaagcggg 60
120 ggggtcttcc agaagaagaa agggccaagg tcacccggg gcctctccag cagcagcaga 120
121 gggcgggcgg cggtgtcgct gctggccggg gcctcgagga aggcgcgggc cagctggggc 180

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122 cgggtctgcg tttccaggag ctgccaccgt tccagggagc aagtcaggcc gggacgttag 240
123 gcctgcgcgc ggaccctcac ttgccaccaa ggacccca aaccccgccc catccttagc 300
124 gcctgcgcgc gaccctcact tgccaccaag acccccacaa accccgcccc atcctgcctt 360
125 acgccccgcc ccaaggctgt tctcccgacc cgggggtccc ccccaagacc gtctctccgc 420
126 cccgccgctt ggtggcgccc gcatgctgcc cggatataaa gggtcggccc cacatcccag 480
127 ggaccagcga gcggccttga gaggtctctg ctcttgcttc ttaggcggcc cgaggacgcc 540
128 atggccgagt gcccgacact                                     560
130 <210> SEQ ID NO: 4
131 <211> LENGTH: 108
132 <212> TYPE: PRT
133 <213> ORGANISM: Artificial Sequence
135 <220> FEATURE:
136 <223> OTHER INFORMATION: MTCPl protein
W--> 138 <221> NAME/KEY: SITE
139 <222> LOCATION: 108
140 <223> OTHER INFORMATION: Xaa = any amino acid
W--> 142 <221> VARIANT
143 <222> LOCATION: 108
144 <223> OTHER INFORMATION: Xaa = Any Amino Acid
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147 <222> LOCATION: 108
148 <223> OTHER INFORMATION: Xaa = Any Amino Acid
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151 Met Ala Gly Glu Asp Val Gly Ala Pro Pro Asp His Leu Trp Val His
152 1 5 10 15
153 Gln Glu Gly Ile Tyr Arg Asp Glu Tyr Gln Arg Thr Trp Val Ala Val
154 20 25 30
155 Val Glu Glu Glu Thr Ser Phe Leu Arg Ala Arg Val Gln Gln Ile Gln
156 35 40 45
157 Val Pro Leu Gly Asp Ala Ala Arg Pro Ser His Leu Leu Thr Ser Gln
158 50 55 60
159 Leu Pro Leu Met Trp Gln Leu Tyr Pro Glu Glu Arg Tyr Met Asp Asn
160 65 70 75 80
161 Asn Ser Arg Leu Trp Gln Ile Gln His His Leu Met Val Arg Gly Val
162 85 90 95
W--> 163 Gln Glu Leu Leu Lys Leu Leu Pro Asp Asp Xaa
164 100 105
167 <210> SEQ ID NO: 5
168 <211> LENGTH: 4922
169 <212> TYPE: DNA
170 <213> ORGANISM: Artificial Sequence
172 <220> FEATURE:
173 <223> OTHER INFORMATION: genomic DNA of TCL-1
W--> 175 <221> NAME/KEY: misc_feature
176 <222> LOCATION: (1)...(4922)
177 <223> OTHER INFORMATION: n = A,T,C or G
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180 gtcgacttgt gaktccmag magaggccca gaagtcccgc tccggcaaa cggaggggaa 60
181 gcgggggggg tcttccaaga agaagaaagg gcccaagggt caacccccgc tgccttctcc 120

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182 agcagcaagc aagagggcgg cgggtcgggt gtcgctgctg gccggggccc tccgaggaaa 180
183 ggcgcggrcc agctggggcc gggctctgctg tcccaggagc tgccaccgtt ccaggggagca 240
184 agtcaggccg ggacgttagc gctgcgcggg gaccctcact tgccaccaag rmccccacaa 300
185 accccgcccc atcctgyctt acgccccgcc ccaaggtcgg ttctccccga cccgggggtc 360
W--> 186 ccgcccccaa ggnccgtcct ccccgcccc gccggttggg ggcggccgca tgcgtccccg 420
187 atataaaggg tcggccccac tccccaggga ccagcgagcg gccttgagag gctctggctc 480
188 ttgcttctta ggcggccccga ggacgccatg gccgagtgcc cgacactcgg ggaggcagtc 540
189 accgaccacc cggaccgcct gtgggcctgg gagaagttcg tgtatttggg cgagaagcag 600
190 macgcctgcc tgcccttaac catcgaggta caaccacctt tggagcggat ggcgargcag 660
191 caggggcasc ccctgggagc ttgggatncc ctaggaaggg cgaggactca aggagcactc 720
192 actatggggc agggaggatc ccccacagat kaagccactt ttggagccgg sctctkgagg 780
193 gatgaatagg agttcctcca ggcaggggaag aagggtggga aaaccccaaa ggaatgtcgg 840
194 tcaaaggggt ggacccagtg cctgtggagt gtgactataa tgttgactac agcaggcatt 900
195 ttctgggctt cggggctcta atccttaaaa atgggtatct ctaagtgact catccatag 960
196 gccgattatt ggaatcatct caggtgggtc ccagaaatct gtatttttaa aaagaacccw 1020
197 cmacagttta gggccaacc caggcataac caaacactg gcctaagagt tgtgaagtat 1080
198 tttccacact accctctggg ctttatttaa gamaacaaa ttaacaagt gatgtcgtag 1140
199 tataagcgcc ggtantkgaa ycaatattga cttttttaat gtgtgatgcc ttaagatggg 1200
200 tccttaatcc atgttaagnt tttgttaaag aaatagataa gtcttttaca agtatttggg 1260
201 tttactcaat gaaaaagagt canaaaatgt tcaaactctc tccaaacata cactgaagaa 1320
202 agcataaaaa ttannaaata tattagaaca cgtatgtcca gtagcaawca maaattattg 1380
203 agtggtgagt gtgtctctac agatgggaaa ctgaggcaca cmaaattgtac atttgtccga 1440
204 ggtaagattg ctagtaggta atggggttgg aattctaggc tcttaaccac caaaaatct 1500
205 gcatttttat tggcatttca attttttaa tatgttttta ctttaaaaat caagttaa 1560
206 acttactttt ttaaaatcaa aatttgaaga aataatttga agattcagtg gatttctttt 1620
207 tttaaatctc tgagaaatct cttccctyca acgtgacacc maaaccmgag aaccagacag 1680
208 tttttcataa aatcatgaaa catgcyccmc maaaaataac ccactasca actgtgggac 1740
209 agattttgcc tcacatcatt gaaaaggcca gcawtctttt tctctctttc tttctttgkt 1800
210 gttttttttt tttcctgtag awacagggtc tcgctctgtg acccaggctg gtctyaaact 1860
211 cctggcctca agcgatcctc ctgcctctgc cttccaaagc actggaatta caagtgtgag 1920
212 ccgctgcaac ccgccagaaa aaagtgtgccc tttcatggcc ctgtctgggt ggctagacac 1980
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215 gatgggtgga tgsctgscag ggagggatc cggtkttcct gcgcctggag aanccctgcc 2160
216 aagcggaacc tgaaagtatn ccctgtcctt ttcttctcct nagataaagg ataggttaca 2220
217 gttnnnggtg ctcttgctgc gggaagacgt cgtcctgggg aggcctatga cccccaccna 2280
218 gataggccca agcctgctgc ctatcatgtg gcagctctac cctgatggac gataccgatc 2340
219 ctgagactcc agtttctggc gcttagtgta ccacatcaag gtgagtgtct ttctcccaga 2400
220 ggteccatcg ktgatcttgg gtttccctc cymatgtct gsccttagtg gtttaycttc 2460
221 ccyccatccc agtssgcaaa agcattwaaa aratggggga nrtrwacmas tgcagatttc 2520
222 tanaggactt taccagagag aaganagatc cnttgagggt tctaanagaa ccctacctcc 2580
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224 aaggctgggt ggaggagggr caktctccaa gasccctga aatcctcaca cctgggttcc 2700
225 tacctgctgt ttccagctag gggaagscsc aggagttagg aatggaggga gtggagggct 2760
226 ctggccgatc aatgccttct ctctctctct gcctctcaga ttgacggcgt ggaggacatg 2820
227 cttctcgagc tgctgccaga tgactgatgt atggtgagct ccactggagc ctgaccctc 2880
228 ttagtccaca gtggctgtat cagaaagaaa gaccaccct tctccatgaa ggcagtgtca 2940
229 accctcccc gactgctgcc atctgagggt ccctagggat gggagaggct tctggaggc 3000
230 actcatgtct cccttaccac ttcgggagcc aagggttttg gtaggcagcc ccctttatcg 3060

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231 cagctgctca tatctataaa gtacttcaca agtttcagct ggcactttca ttttaccatt 3120
232 gctttttttt tctttgggag atgagtcctg ctctgtggcc caggctagag tgtagtgggt 3180
233 gcaatctcag ctcaactgaaa gctctgcctc ccgggttcac accattctcc tgccctcagcc 3240
234 ctcgagtag ctgggactac aggcgcgcgc caccacacct ggctaatttt tttttttttw 3300
235 ttwtwttttt tagtagagmc ggggtttcac cgtgttagcc aggatggtct cgatctcctg 3360
236 acctcatgat ctgcccgcct cggcctccca aagtgtctggg attacaggca tgagccacca 3420
237 cgtccggcct taccattgct ttattaaata agcactggtg cttgattata tcagctgagc 3480
238 cagatattag atacgctatt gagttttgrg gaaataagag taccaaaact cagaaatgag 3540
239 ttgaagtata gtgacatctt cagattacag acccagggtg cagaatttgc cttgggtcag 3600
240 aaggcctctg ggggccatcc ctgaccacta ggcttccac ttagacctgc tccagcagca 3660
241 ccaccctctg scactgcctg gtcttttctc tcaccttga ttctgtcttc tttgtcctt 3720
242 ctccaggtct tgggagcacc tgtctctttt caccccaggg cctgagcctg gccagcctac 3780
243 aatgggggat ttgtgtttct gttcaccttc gtttactatg bctgtgtctt ctccaccacg 3840
244 ctgggtctg ggaggaatgg acagacagag gatgagctct acccrgggcc tgsaggacct 3900
245 gtctgtgagm ccactctgct cgccttaga cctacsactc cwrccgasga ggatnccant 3960
246 tggaagagct tcttnnagg gncnaanaan anctgtgcgt nggcttttct cagctggatg 4020
247 atggtcntna gcctctttct gtcccttctg tccctcacag cactagtatt tnatgttgca 4080
248 caccactca gctccgtgaa tttgtgagaa cacaaccgat tcacctgagc aggacctctg 4140
249 aaacctgga ccagtgtct cacatggtgc tacgctgca tgtaaacacg cctncaaacg 4200
250 ctgctgcck gtraacacgm sksyrmacag stgmswrcc gtaaacacgc ctgcaaacgc 4260
251 tgctgcca cacaggttca cgtgcagtc aaggaaagrm ctgaaarrag cccttatctg 4320
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253 aggcggcgca gccctgtgga tgagccctca gaacccttg gttgcccacg tggaaaagg 4440
254 atagaggttg ggtttcccc cttttataga tggtcacgca cctgggtgtt acaaagtgt 4500
255 atgtggcatg aatacttgnt gtnatgattg attaaatgca agatagtta tctaacttcg 4560
256 tgcggaatca gcttctatcc ttgncttaga ttctgggtgga gagaagtgan aataggcagn 4620
257 cccanataa anaatattca ngggatttat tttatnttc cttttggng atnngggact 4680
258 acattntn nccccgtnta atccaatgnt taaanccca gtgttcttg aggnctacg 4740
259 tcgaanacca ttggngtang caacctcaa atttttnngt tgnnaattnc cngttttcca 4800
260 gagncccc cntnctccat cttntctcn gccnccctn nccctccnca ntcccnangt 4860
261 tnccctcgn cccagtcagt tctttctcn nctttanccg ntatntcac cagnttctt 4920
262 ct 4922
264 <210> SEQ ID NO: 6
265 <211> LENGTH: 20
266 <212> TYPE: DNA
267 <213> ORGANISM: Artificial Sequence
269 <220> FEATURE:
270 <223> OTHER INFORMATION: p9A primer
272 <400> SEQUENCE: 6
273 tgctgccaga tgactgatgt 20
275 <210> SEQ ID NO: 7
276 <211> LENGTH: 20
277 <212> TYPE: DNA
278 <213> ORGANISM: Artificial Sequence
280 <220> FEATURE:
281 <223> OTHER INFORMATION: Rev III primer
283 <400> SEQUENCE: 7
284 caaatggaat ctccttggc 20
286 <210> SEQ ID NO: 8

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RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : F:\3589.1017-001 Seq List.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; Xaa Pos. 108
Seq#:5; N Pos. 373,688,1155,1219,1283,1334,1335,2153,2180,2201,2224,2225
Seq#:5; N Pos. 2279,2501,2523,2545,2553,2566,2592,2599,3955,3959,3975,3976
Seq#:5; N Pos. 3982,3984,3987,3990,3992,4001,4027,4029,4072,4194,4372,4519
Seq#:5; N Pos. 4523,4584,4610,4620,4626,4632,4641,4657,4669,4673,4674,4686
Seq#:5; N Pos. 4688,4690,4691,4698,4709,4715,4734,4736,4746,4755,4759,4777
Seq#:5; N Pos. 4778,4783,4784,4789,4792,4804,4812,4814,4824,4825,4830,4835
Seq#:5; N Pos. 4840,4841,4848,4851,4856,4858,4862,4869,4890,4891,4897,4901
Seq#:5; N Pos. 4903,4906,4914
Seq#:12; Xaa Pos. 113

VERIFICATION SUMMARY

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Input Set : F:\3589.1017-001 Seq List.txt

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L:30 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:33 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:138 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:142 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:146 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:150 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:96
L:175 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:179 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:360
M:341 Repeated in SeqNo=5
L:338 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:342 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:346 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:350 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
L:365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:112